

0590
25/3

#6



OIPE

EX-111111

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/071,879

DATE: 05/16/2002

TIME: 13:03:09

Input Set : A:\LEX-0299-USA SEQLIST.txt

Output Set: N:\CRF3\05162002\J071879.raw

4 <110> APPLICANT: Turner, C. Alexander Jr.
 5 Yu, Xuanchuan
 6 Friddle, Carl Johan
 7 Miranda, Maricar
 8 Gerhardt, Brenda
 9 Mathur, Brian
 11 <120> TITLE OF INVENTION: Novel Human Ig-Domain Proteins and Polynucleotides Encoding
 the Same
 13 <130> FILE REFERENCE: LEX-0299-USA
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/071,879
 C--> 15 <141> CURRENT FILING DATE: 2002-02-08
 15 <150> PRIOR APPLICATION NUMBER: US 60/267,583
 16 <151> PRIOR FILING DATE: 2001-02-09
 18 <160> NUMBER OF SEQ ID NOS: 11
 20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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 23 <211> LENGTH: 936
 24 <212> TYPE: DNA
 25 <213> ORGANISM: homo sapiens
 27 <400> SEQUENCE: 1
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 30 tttaccgtcc tatctgcagt cggctacttt cagtggcaga agaggccaca tctgcttcct 180
 31 gtaggccctc tgggcagaag catgcgctgg tgtctcctcc tgatctgggc ccaggggctg 240
 32 aggcaggctc ccctcgccctc aggaatgatg acaggcaca tagaaacaac gggaacatt 300
 33 tctgcagaga aagggtggctc tatcatctta caatgtcacc tctcctccac caccgcacaa 360
 34 gtgacccagg tcaactggga gcagcaggac cagcttctgg ccatttgtaa tgctgacttg 420
 35 ggggtggcaca tctccccatc cttcaaggat cgagtggccc caggtcccgg cctgggcctc 480
 36 accctccagt cgctgaccgt gaacgataca ggggagtact tctgcatcta tcacacctac 540
 37 cctgatggga cgtacactgg gagaatcttc ctggaggctc tagaaagctc agtggctgag 600
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 40 tctgtggaag gtgacctcag gagaaaatca gctggacagg aggaatggag cccagtgct 780
 41 ccctcacccc caggaagctg tgtccaggca gaagctgcac ctgctgggct ctgtggagag 840
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 46 <211> LENGTH: 311
 47 <212> TYPE: PRT
 48 <213> ORGANISM: homo sapiens
 50 <400> SEQUENCE: 2
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 53 Thr Leu Cys Val Phe Asn Met Val Phe Ala Lys Leu Gly Phe Ser Glu

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55 Thr Val Phe Ser Gln Arg Leu Ser Phe Thr Val Leu Ser Ala Val Gly
56          35          40          45
57 Tyr Phe Gln Trp Gln Lys Arg Pro His Leu Leu Pro Val Gly Pro Leu
58          50          55          60
59 Gly Arg Ser Met Arg Trp Cys Leu Leu Leu Ile Trp Ala Gln Gly Leu
60 65          70          75          80
61 Arg Gln Ala Pro Leu Ala Ser Gly Met Met Thr Gly Thr Ile Glu Thr
62          85          90          95
63 Thr Gly Asn Ile Ser Ala Glu Lys Gly Gly Ser Ile Ile Leu Gln Cys
64          100          105          110
65 His Leu Ser Ser Thr Thr Ala Gln Val Thr Gln Val Asn Trp Glu Gln
66          115          120          125
67 Gln Asp Gln Leu Leu Ala Ile Cys Asn Ala Asp Leu Gly Trp His Ile
68          130          135          140
69 Ser Pro Ser Phe Lys Asp Arg Val Ala Pro Gly Pro Gly Leu Gly Leu
70 145          150          155          160
71 Thr Leu Gln Ser Leu Thr Val Asn Asp Thr Gly Glu Tyr Phe Cys Ile
72          165          170          175
73 Tyr His Thr Tyr Pro Asp Gly Thr Tyr Thr Gly Arg Ile Phe Leu Glu
74          180          185          190
75 Val Leu Glu Ser Ser Val Ala Glu His Gly Ala Arg Phe Gln Ile Pro
76          195          200          205
77 Leu Leu Gly Ala Met Ala Ala Thr Leu Val Val Ile Cys Thr Ala Val
78          210          215          220
79 Ile Val Val Val Ala Leu Thr Arg Lys Lys Lys Ala Leu Arg Ile His
80 225          230          235          240
81 Ser Val Glu Gly Asp Leu Arg Arg Lys Ser Ala Gly Gln Glu Glu Trp
82          245          250          255
83 Ser Pro Ser Ala Pro Ser Pro Pro Gly Ser Cys Val Gln Ala Glu Ala
84          260          265          270
85 Ala Pro Ala Gly Leu Cys Gly Glu Gln Arg Gly Glu Asp Cys Ala Glu
86          275          280          285
87 Leu His Asp Tyr Phe Asn Val Leu Ser Tyr Arg Ser Leu Gly Asn Cys
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89 Ser Phe Phe Thr Glu Thr Gly
90 305          310
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95 <212> TYPE: DNA
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101 caggaccagc ttctggccat ttgtaatgct gacttggggg ggcacatctc cccatccttc 180
102 aaggatcgag tggcccaggg tcccggcctg ggccctaccc tccagtcgct gaccgtgaac 240
103 gatacagggg agtacttctg catctatcac acctaccctg atgggacgta cactgggaga 300
104 atcttctctg aggtcctaga aagctcagtg gctgagcacg gtgccagggt ccagattcca 360
105 ttgcttgagg ccattggccg cagctggtg gtcattctga cagcagtcac cgtgggtggtc 420

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107 aaatcagctg gacaggagga atggagcccc agtgctccct caccgccagg aagctgtgtc 540
108 caggcagaag ctgcacctgc tgggctctgt ggagagcagc ggggagagga ctgtgccgag 600
109 ctgcatgact acttcaatgt cctgagttac agaagcctgg gtaactgcag cttcttcaca 660
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114 <212> TYPE: PRT

115 <213> ORGANISM: homo sapiens

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120 Gly Gly Ser Ile Ile Leu Gln Cys His Leu Ser Ser Thr Thr Ala Gln

121 20 25 30

122 Val Thr Gln Val Asn Trp Glu Gln Gln Asp Gln Leu Leu Ala Ile Cys

123 35 40 45

124 Asn Ala Asp Leu Gly Trp His Ile Ser Pro Ser Phe Lys Asp Arg Val

125 50 55 60

126 Ala Pro Gly Pro Gly Leu Gly Leu Thr Leu Gln Ser Leu Thr Val Asn

127 65 70 75 80

128 Asp Thr Gly Glu Tyr Phe Cys Ile Tyr His Thr Tyr Pro Asp Gly Thr

129 85 90 95

130 Tyr Thr Gly Arg Ile Phe Leu Glu Val Leu Glu Ser Ser Val Ala Glu

131 100 105 110

132 His Gly Ala Arg Phe Gln Ile Pro Leu Leu Gly Ala Met Ala Ala Thr

133 115 120 125

134 Leu Val Val Ile Cys Thr Ala Val Ile Val Val Val Ala Leu Thr Arg

135 130 135 140

136 Lys Lys Lys Ala Leu Arg Ile His Ser Val Glu Gly Asp Leu Arg Arg

137 145 150 155 160

138 Lys Ser Ala Gly Gln Glu Glu Trp Ser Pro Ser Ala Pro Ser Pro Pro

139 165 170 175

140 Gly Ser Cys Val Gln Ala Glu Ala Ala Pro Ala Gly Leu Cys Gly Glu

141 180 185 190

142 Gln Arg Gly Glu Asp Cys Ala Glu Leu His Asp Tyr Phe Asn Val Leu

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144 Ser Tyr Arg Ser Leu Gly Asn Cys Ser Phe Phe Thr Glu Thr Gly

145 210 215 220

148 <210> SEQ ID NO: 5

149 <211> LENGTH: 1821

150 <212> TYPE: DNA

151 <213> ORGANISM: homo sapiens

153 <400> SEQUENCE: 5

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155 ttcatgggat ccaccattgg ctgccccgct cgctgtgagt gctctgcca gaacaaatct 120

156 gttagctgtc acagaaggcg attgatcgcc atcccagagg gcattcccat cgaaaccaa 180

157 atcttggacc tcagtaaaaa caggctaaaa agcgtcaacc ctgaagaatt catatcatat 240

158 cctctgctgg aagagataga cttgagtgac aacatcattg ccaatgtgga accaggagca 300

159 ttcaacaata tctttaacct gcgttccttc cgcctaaaag gcaatcgtct aaagctgggtc 360

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160 cctttggggag tattcacggg gctgtccaat ctactaagc ttgacattag tgagaataag 420
161 attgtcattt tactagacta catgttccaa gatctacata acctgaagtc tctagaagtg 480
162 ggggacaatg atttggttta tatatcacac agggcattca gtgggcttct tagcttggag 540
163 cagctcaccc tggagaaatg caacttaaca gcagtaccaa cagaagccct ctcccacctc 600
164 cgcagcctca tcagcctgca tctgaagcat ctcaatatca acaatatgcc tgtgtatgcc 660
165 tttaaaagat tgttccacct gaaacaccta gagattgact attggccttt actggatatg 720
166 atgcctgcca atagcctcta cgggtctcaac ctacatccc tttagtcac caacaccaat 780
167 ctgtctactg taaccttcct tgcctttaa cacctggtat acctgactca ccttaacctc 840
168 tcctacaatc ccatcagcac tattgaagca ggcattgtct ctgacctgat ccgccttcag 900
169 gagcttcata tagtgggggc ccagcttcgc accattgagc ctactcctt ccaagggctc 960
170 cgcttcctac gcgtgctcaa tgtgtctcag aacctgctgg aaactttgga agagaatgtc 1020
171 ttctcctccc ctagggtctt ggaggtcttg agcattaaca acaacctctt ggctgtgac 1080
172 tgccgccttc tctggatctt gcagcgacag cccacctgc agtttggtgg ccagcaacct 1140
173 atgtgtgctg gccagacac catcogtgag aggtctttca aggatttoca tagcactgcc 1200
174 ctttcttttt actttacctg caaaaaaccc aaaatccgtg aaaagaagtt gcagcatctg 1260
175 ctagtagatg aagggcgagc agtccagcta gaatgcagtg cagatggaga cccgcagcct 1320
176 gtgatttcct gggtgacacc ccgaaggcgt ttcacacca ccaagtccaa tggaagagcc 1380
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178 tatgtttgca tcgctagcaa tgcgtctggg aatgatacct tcacagcctc cttactgtg 1500
179 aaaggattcg cttcagatcg ttttctttat gcgaacagga cccctatgta catgaccgac 1560
180 tccaatgaca ccatttccaa tggcaccaat gccaatactt tttccctgga ccttaaaaca 1620
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182 cttctccttt ttgtgtggag ccgagggaaa ggcaagcaca aaaacagcat tgaccttgag 1740
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188 <212> TYPE: PRT
189 <213> ORGANISM: homo sapiens
191 <400> SEQUENCE: 6
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195 20 25 30
196 Glu Cys Ser Ala Gln Asn Lys Ser Val Ser Cys His Arg Arg Arg Leu
197 35 40 45
198 Ile Ala Ile Pro Glu Gly Ile Pro Ile Glu Thr Lys Ile Leu Asp Leu
199 50 55 60
200 Ser Lys Asn Arg Leu Lys Ser Val Asn Pro Glu Glu Phe Ile Ser Tyr
201 65 70 75 80
202 Pro Leu Leu Glu Glu Ile Asp Leu Ser Asp Asn Ile Ile Ala Asn Val
203 85 90 95
204 Glu Pro Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Ser Leu Arg Leu
205 100 105 110
206 Lys Gly Asn Arg Leu Lys Leu Val Pro Leu Gly Val Phe Thr Gly Leu
207 115 120 125
208 Ser Asn Leu Thr Lys Leu Asp Ile Ser Glu Asn Lys Ile Val Ile Leu
209 130 135 140
210 Leu Asp Tyr Met Phe Gln Asp Leu His Asn Leu Lys Ser Leu Glu Val

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211 145          150          155          160
212 Gly Asp Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu
213          165          170          175
214 Leu Ser Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ala Val
215          180          185          190
216 Pro Thr Glu Ala Leu Ser His Leu Arg Ser Leu Ile Ser Leu His Leu
217          195          200          205
218 Lys His Leu Asn Ile Asn Asn Met Pro Val Tyr Ala Phe Lys Arg Leu
219          210          215          220
220 Phe His Leu Lys His Leu Glu Ile Asp Tyr Trp Pro Leu Leu Asp Met
221 225          230          235          240
222 Met Pro Ala Asn Ser Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Val
223          245          250          255
224 Thr Asn Thr Asn Leu Ser Thr Val Pro Phe Leu Ala Phe Lys His Leu
225          260          265          270
226 Val Tyr Leu Thr His Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile
227          275          280          285
228 Glu Ala Gly Met Phe Ser Asp Leu Ile Arg Leu Gln Glu Leu His Ile
229          290          295          300
230 Val Gly Ala Gln Leu Arg Thr Ile Glu Pro His Ser Phe Gln Gly Leu
231 305          310          315          320
232 Arg Phe Leu Arg Val Leu Asn Val Ser Gln Asn Leu Leu Glu Thr Leu
233          325          330          335
234 Glu Glu Asn Val Phe Ser Ser Pro Arg Ala Leu Glu Val Leu Ser Ile
235          340          345          350
236 Asn Asn Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Ile Leu Gln
237          355          360          365
238 Arg Gln Pro Thr Leu Gln Phe Gly Gly Gln Gln Pro Met Cys Ala Gly
239          370          375          380
240 Pro Asp Thr Ile Arg Glu Arg Ser Phe Lys Asp Phe His Ser Thr Ala
241 385          390          395          400
242 Leu Ser Phe Tyr Phe Thr Cys Lys Lys Pro Lys Ile Arg Glu Lys Lys
243          405          410          415
244 Leu Gln His Leu Leu Val Asp Glu Gly Gln Thr Val Gln Leu Glu Cys
245          420          425          430
246 Ser Ala Asp Gly Asp Pro Gln Pro Val Ile Ser Trp Val Thr Pro Arg
247          435          440          445
248 Arg Arg Phe Ile Thr Thr Lys Ser Asn Gly Arg Ala Thr Val Leu Gly
249          450          455          460
250 Asp Gly Thr Leu Glu Ile Arg Phe Ala Gln Asp Gln Asp Ser Gly Met
251 465          470          475          480
252 Tyr Val Cys Ile Ala Ser Asn Ala Ala Gly Asn Asp Thr Phe Thr Ala
253          485          490          495
254 Ser Leu Thr Val Lys Gly Phe Ala Ser Asp Arg Phe Leu Tyr Ala Asn
255          500          505          510
256 Arg Thr Pro Met Tyr Met Thr Asp Ser Asn Asp Thr Ile Ser Asn Gly
257          515          520          525
258 Thr Asn Ala Asn Thr Phe Ser Leu Asp Leu Lys Thr Ile Leu Val Ser
259          530          535          540

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VERIFICATION SUMMARY

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Input Set : A:\LEX-0299-USA SEQLIST.txt

Output Set: N:\CRF3\05162002\J071879.raw

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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date